Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims

Claims 1-2 (canceled)

3. (amended) The method of claims ~~1 or 2~~ 127, wherein at least about 100 samples are screened for presence of the one or more component of interest in less than an hour.

4. (amended) The method of claim ~~1~~ 127, wherein at least about 200 samples are screened for presence of the one or more ~~non-column-separated~~ component of interest in less than an hour.

5. (amended) The method of claim ~~1~~ 127, wherein at least about 500 ~~non-column-separated~~ samples are screened for presence of the one or more component of interest in less than an hour.

6. (amended) The method of claim ~~1~~ 127, wherein at least about 1000 samples are screened for the presence of the one or more component of interest in about 1 day.

Claims 7-22 (canceled)

23. (amended) The method of claim ~~1~~ 127 , wherein performing flow injection analysis using electrospray tandem mass spectrometry comprises performing a method selected from the group consisting of neutral loss mass spectrometry and parent ion mass spectrometry.

24. (Original) The method of claim 23, comprising performing the neutral loss mass spectrometry or the parent ion mass spectrometry on a triple quadrupole mass spectrometer.

25. (previously presented) The method of claim 24, wherein performing the neutral loss mass spectrometry comprises:

(a) scanning the one or more component of interest in a first quadrupole at a specified mass range;

(b) fragmenting the one or more component of interest in a second quadrupole by collision induced dissociation, thereby producing one or more neutral fragments and one or more daughter ion; and,

(c) detecting the one or more daughter ion.

26. (previously presented) The method of claim 24, wherein performing the parent ion mass spectrometry comprises:

(a) scanning the one or more component of interest in a first quadrupole;

(b) fragmenting the one or more component of interest in a second quadrupole by collision induced dissociation; and,

(c) scanning a third quadrupole at a specified mass.

Claims 27-71 (canceled)

72. (currently amended) The method of claim ~~1~~ 127, wherein ~~purifying in~~ step ~~(iv)~~ (iii) comprises using centrifugation.

73. (currently amended) The method of claim ~~1~~ 127, wherein ~~purifying in~~ step (iii) comprises using filtration.

Claims 74-76 (canceled)

77. (currently amended) The method of claim ~~1~~ 127 , wherein an automatic sampler transports ~~purified~~ samples from step (iii) to the mass spectrometer for injection and analysis at a rate of at least 100 samples an hour.

78. (currently amended) The method of claim ~~1~~ 127 , wherein 5 to 100 samples are pooled before performing flow-injection analysis using electrospray tandem mass spectrometry.

Claims 79-105 (canceled)

106. (currently amended) The method of claim ~~105~~ 136, wherein at least about 100 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

107. (currently amended) The method of claim ~~105~~ 136, wherein at least about 200 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

108. (currently amended) The method of claim ~~105~~ 136, wherein at least about 500 samples are screened for presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in less than an hour.

109. (currently amended) The method of claim ~~105~~ 136, wherein at least about 1000 samples are screened for the presence of the product(s) of an enzymatic reaction or enzyme substrate(s) in about 1 day.

110. (currently amended) The method of claim ~~105~~ 136 , wherein the ~~non-column-separated samples comprise cell lysate~~ cells in step (iii) are lysed.

Claims 111-114 (canceled)

115. (currently amended) The method of claim~~105~~ 136, ~~wherein the one or more component of interest comprises the enzyme substrate and the product of an enzymatic reaction, the method~~ further comprising simultaneously quantifying the amount of the product(s) of an enzyme reaction and the enzyme substrate(s).

116. (currently amended) The method of claim ~~105~~ 136 , wherein performing flow injection analysis using electrospray tandem mass spectrometry comprises performing a method selected from the group consisting of neutral loss mass spectrometry and parent ion mass spectrometry.

117. (previously presented) The method of claim 116, comprising performing the neutral loss mass spectrometry or the parent ion mass spectrometry on a triple quadrupole mass spectrometer.

118 (amended) The method of claim 117, wherein performing the neutral loss mass spectrometry comprises:

(a) scanning the ~~one or more component of interest~~ product(s) of the enzymatic reaction and/or enzyme substrate in a first quadrupole at a specified mass range;

(b) fragmenting the ~~one or more component of interest~~ product(s) of the enzymatic reaction and/or enzyme substrate in a second quadrupole by collision induced dissociation, thereby producing one or more neutral fragments and one or more daughter ion; and,

(c) detecting the one or more daughter ion.

119. (amended) The method of claim 117, wherein performing the parent ion mass spectrometry comprises:

(a) scanning the ~~one or more component of interest~~ product(s) of the enzymatic reaction and/or enzyme substrate in a first quadrupole;

(b) fragmenting the ~~one or more component of interest~~ product(s) of the enzymatic reaction and/or enzyme substrate in a second quadrupole by collision induced dissociation; and,

(c) scanning a third quadrupole at a specified mass.

Claims 120-124 (canceled)

125. (currently amended) The method of claim ~~105~~ 136, wherein an automatic sampler transports the ~~purified~~ samples from ~~purification~~ step (iv) to the mass spectrometer for injection and analysis at a rate of at least 100 samples an hour.

126. (currently amended) The method of claim ~~105~~ 136, wherein 5 to 100 samples are pooled before performing flow-injection analysis using electrospray tandem mass spectrometry.

127. (new) A method of performing high throughput mass spectrometry screening, the method comprising:

(i) providing cells that have been transfected or transformed with one or more members of a library of related genes;

(ii) growing the cells in vitro in a biological matrix to express said members of the library of related genes;

(iii) separating the cells or cell debris thereof from one or more component of interest using centrifugation or filtration in a parallel fashion to provide samples comprising the component(s) of interest;

(iv) performing flow-injection analysis using electrospray tandem mass spectrometry on the samples from step (iii) to obtain mass-to-charge ratio data for the component of interest,

wherein the component(s) of interest is selected from the group consisting of an inorganic ion, a secondary metabolite, a protein binding molecule, a carbohydrate, a carbohydrate binding molecule, an enzyme, an enzyme substrate, a product of an enzyme catalyzed reaction, a nucleic acid, and a product of a nucleic acid catalyzed reaction, and

wherein the component(s) of interest has not undergone chromatographic separation prior to step (iv).

128. (new) The method of claim 127, wherein the cells are lysed prior to step (iii).

129. (new) The method of claim 127, wherein the cells are permeabilized prior to step (iii).

130. (new) The method of claim 127, wherein the component(s) of interest is obtained from cell supernatant.

131. (new) The method of claim 127, wherein the component(s) of interest is a product of an enzymatic reaction.

132. (new) The method of claim 127, wherein the cells are bacterial cells.

133. (new) The method of claim 127, wherein the cells are eukaryotic cells.

134. (new) The method of claim 127, wherein step (iii) is performed in a volatile buffer, a buffer that reduces concentration of ionic species, or an organic solvent.

135. (new) The method of claim 131, further comprising simultaneously quantifying the amount of the product(s) of the enzymatic reaction and an enzyme substrate.

136. (new) A method of performing high throughput mass spectrometery screening, the method comprising:

(i) providing cells that have been transfected or transformed with one or more members of a library of related enzyme encoding genes;

(ii) growing the cells in vitro in a biological matrix to express said members of the library of related enzyme encoding genes;

(iii) contacting the cells with one or more enzyme substrates to initiate formation of one or more products of an enzymatic reaction;

(iv) separating the cells or cell debris thereof from the product of the enzymatic reaction and/or enzyme substrate using centrifugation or filtration in a parallel fashion to provide samples comprising the product(s) of the enzymatic reaction and/or enzyme substrate(s); and

(v) performing flow-injection analysis using electrospray tandem mass spectrometry on the samples from step (iv) to obtain mass-to-charge ratio data for the product(s) of the enzymatic reaction and/or enzyme substrate(s),

wherein the product(s) of the enzymatic reaction and enzyme substrate(s) have not undergone chromatographic separation prior to step (v).

137. (new) The method of claim 136, wherein the cells in step (iii) are lysed cells.

138. (new) The method of claim 136, wherein the cells in step (iii) are permeabilized cells.

139. (new) The method of claim 136, wherein the cells are bacterial cells.

140. (new) The method of claim 136, wherein the cells are eukaryotic cells.

141. (new) The method of claim 136, wherein step (iii) comprises using centrifugation.

142. (new) The method of claim 136, wherein step (iii) comprises using filtration.

143. (new) The method of claim 136, wherein step (iv) is performed in a volatile buffer, a buffer than reduces concentration of ionic species, or an organic solvent.